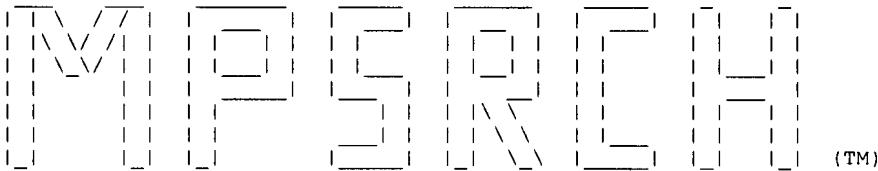


08/476567  
attachment to  
Report 15

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Fri Aug 8 16:02:47 1997; MasPar time 1175.28 Seconds  
1326.024 Million cell updates/sec

Tabular output not generated.

Title: >N70819  
Description: (1-1419) from us08476567.seq  
Perfect Score: 1419  
N.A. Sequence: 1 ccgagccgagaatgggagta.....aatagaggagtcaagttctt 1419  
Comp: ggctcggtcttaccctcat.....ttatctcctcagttcaagaa

Scoring table: TABLE default  
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 362067 seqs, 549138275 bases x 2

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database: embl-new3  
1:BCT 2:FUN 3:GEN1 4:GEN2 5:HTG1 6:HTG2 7:HUM 8:INV  
9:ORG 10:MAM 11:VRT 12:PLN 13:PRO 14:ROD 15:SYN 16:UNC  
17:VIR

Database: genbank99  
18:BCT1 19:BCT2 20:BCT3 21:BCT4 22:BCT5 23:BCT6 24:BCT7  
25:BCT8 26:BCT9 27:BCT10 28:BCT11 29:GEN1 30:GEN2  
31:GEN3 32:HTG1 33:HTG2 34:HTG3 35:INV1 36:INV2 37:INV3  
38:INV4 39:INV5 40:INV6 41:INV7 42:INV8 43:INV9 44:INV10  
45:INV11 46:MAM1 47:MAM2 48:MAM3 49:VRT1 50:VRT2 51:VRT3  
52:VRT4 53:PAT1 54:PAT2 55:PAT3 56:PAT4 57:PAT5 58:PHG  
59:PLN1 60:PLN2 61:PLN3 62:PLN4 63:PLN5 64:PLN6 65:PLN7  
66:PLN8 67:PLN9 68:PLN10 69:PLN11 70:PRI1 71:PRI2  
72:PRI3 73:PRI4 74:PRI5 75:PRI6 76:PRI7 77:PRI8 78:PRI9  
79:PRI10 80:PRI11 81:PRI12 82:PRI13 83:PRI14 84:PRI15  
85:ROD1 86:ROD2 87:ROD3 88:ROD4 89:ROD5 90:ROD6 91:ROD7  
92:ROD8 93:STR 94:SYN 95:UNA 96:VRL1 97:VRL2 98:VRL3  
99:VRL4 100:VRL5 101:VRL6 102:VRL7 103:VRL8 104:VRL9  
105:VRL10

Database: genbank-new3  
106:BCT 107:GEN1 108:GEN2 109:HTG1 110:HTG2 111:INV  
112:MAM 113:VRT 114:PHG 115:PLN 116:PRI1 117:PRI2  
118:ROD 119:SYN 120:UNA 121:VRL

Database: u-embl50\_99  
122:part1

Statistics: Mean 11.369; Variance 4.112; scale 2.765

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

\*

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
------------	-------	-------------	--------	----	----	-------------	-----------

1	1419	100.0	1419	53	A12480	cDNA for glutamine sy	0.00e+00
2	1419	100.0	1421	85	CLGSR	Chinese hamster mRNA	0.00e+00
3	1003	70.7	2731	85	MMGSASE	M.musculus mRNA for g	0.00e+00
4	943	66.5	1150	86	MMU09114	Mus musculus glutamat	0.00e+00
5	926	65.3	2787	92	RRGS	Rat mRNA for glutamin	0.00e+00
6	926	65.3	2787	90	RATGLUS	R.norvegicus glutamin	0.00e+00
7	921	64.9	1366	74	HSGLUSYN	Human mRNA for glutam	0.00e+00
8	919	64.8	2727	74	HSGLUS	Human rearranged mRNA	0.00e+00
9	917	64.6	2793	90	RATGLNAB	Rat glutamine synthet	0.00e+00
10	911	64.2	2631	84	S70290	glutamine synthetase	0.00e+00
11	898	63.3	1370	48	SSGLUSYN	S.scrofa mRNA for glu	0.00e+00
12	881	62.1	2925	88	MUSGSA	Mouse intronless glut	0.00e+00
13	812	57.2	3004	77	HSU08626	Human glutamine synth	0.00e+00
14	673	47.4	1838	51	S45408	glutamine synthetase	0.00e+00
15	671	47.3	2728	49	CHKGLN	Chicken retinal gluta	0.00e+00
16	572	40.3	2753	51	SAU04617	Squalus acanthias glu	0.00e+00
17	450	31.7	1617	52	XELXGS	Xenopus laevis mRNA f	0.00e+00
18	449	31.6	1851	88	MUSGLN1	Mouse glutamine synth	0.00e+00
19	342	24.1	2935	43	PALGLUSYN	Paracentrotus lividus	0.00e+00
20	299	21.1	2045	44	PNLGTSYN	Panulirus argus gluta	3.85e-298
21	251	17.7	386	46	BOVGLN	Bovine glutamine synt	8.10e-243
22	247	17.4	2371	90	RATGLUSG6	Rat glutamine synthet	3.15e-238
23	218	15.4	1496	39	DMGS2	D.melanogaster GS2 mR	4.68e-205
24	192	13.5	2162	39	DMGS1	D.melanogaster GS1 mR	1.63e-175
25	181	12.8	649	90	RATGLUSG5	Rat glutamine synthet	4.39e-163
26	172	12.1	2424	60	COGGLN	Colletotrichum gloeos	5.97e-153
27	145	10.2	1354	60	BNGLN	B.napus mRNA for glut	8.77e-123
28	145	10.2	1780	69	YSCGLN1	S.cerevisiae glutamin	8.77e-123
29	145	10.2	10339	65	SC3085	S.cerevisiae chromoso	8.77e-123
30	145	10.2	165536	65	SCCHRXVI	S.cerevisiae chromoso	8.77e-123
31	143	10.1	1450	65	S46513	cytosolic glutamine s	1.45e-120
32	142	10.0	387	90	RATGLUSG2	Rat glutamine synthet	1.86e-119
33	136	9.6	1326	64	RADGS1GC	Raphanus sativus mRNA	8.02e-113
34	136	9.6	1429	63	LSGLUSYN	L.sativa mRNA for glu	8.02e-113
35	135	9.5	1440	62	LJCYTGLSY	L.japonica mRNA for c	1.02e-111
36	134	9.4	1317	69	ZMGS13	Z.mays mRNA gsl-3 for	1.29e-110
37	134	9.4	1490	69	ZMGS14	Z.mays mRNA gsl-4 for	1.29e-110
38	132	9.3	1332	64	PSGSISO	P.sylvestris mRNA for	2.06e-108
39	132	9.3	1350	63	MZEGS1B	Maize mRNA for glutam	2.06e-108
40	132	9.3	1422	63	MZEGS1A	Maize mRNA for glutam	2.06e-108
41	131	9.2	1484	64	RADGS1BB	Raphanus sativus mRNA	2.60e-107
42	130	9.2	1553	63	OSSIGS28	Oryza sativa shoot GS	3.27e-106
43	131	9.2	1649	63	OSSIGS31	Oryza sativa shoot GS	2.60e-107
44	129	9.1	1454	64	PVGSR1	Phaseolus vulgaris mR	4.10e-105
45	129	9.1	1483	69	ZMGS2	Z.mays mRNA gs2 for g	4.10e-105

#### ALIGNMENTS

RESULT 1

LOCUS A12480 1419 bp RNA PAT 09-DEC-1993

DEFINITION cDNA for glutamine synthetase.

ACCESSION A12480

NID g490275

KEYWORDS .

SOURCE long-tailed hamster.

ORGANISM Cricetulus longicaudatus  
Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;  
Vertebrata; Eutheria; Rodentia; Sciurognathi; Myomorpha; Muridae;  
Cricetinae; Cricetulus.

REFERENCE 1 (bases 1 to 1419)

AUTHORS .

TITLE RECOMBINANT DNA SEQUENCES, VECTORS CONTAINING THEM AND METHOD FOR THE USE THEREOF

JOURNAL Patent: WO 8704462-A 1 30-JUL-1987;

FEATURES Location/Qualifiers

source 1..1419  
/organism="Cricetulus longicaudatus"

CDS 145..1266  
/gene="GS gene"  
/codon\_start=1  
/db\_xref="PID:g490276"  
/db\_xref="SWISS-PROT:P04773"

Db	270	ggaactttagtggctccagcacccccaagccaaaggctcaacacgcacatgtacctgc	329
Qy	323	ggaatttttagtggcttagtacccctcagtctgaggctccaacagtgcacatgtatctca	382
Db	330	gacctgtgccatgtccgggaccctttcgcaaggatccaaacaaatttagttctctgtg	389
Qy	383	gcccgttgccatgttcgggacccttccgcaagatccaaacaaagctgtgtctgtg	442
Db	390	aggctctcaaataacaaccggcagtctgcagacacaaatcttcggcacacctgttaggcgg	449
Qy	443	aagttttcaagtacaaccggaaagcctgcagagaccaatttaaggcactcgtgtaaacgg	502
Db	450	ttagggatatggtgtccaaccaggccccctggggatggggcaggatcaccccttc	509
Qy	503	taatggacatggtagcaaccaggccccctggggatggggcaggatatactctqa	562
Db	510	tggggacagatggcatccgtttggctggcccttcaattgtttccctggaccccaagg	569
Qy	563	tggggacagatggggccccctttggggatggcccttcaatggggccctggggcccaagg	622
Db	570	cgtactactgcgggttagggactgacaaaggctatggcagagacattgtggggcccact	629
Qy	623	cgttattactgtgggtggcgcagacaaaggctatggcaggatatcgtggggcact	682
Db	630	accgagcgtgcctgtatgctgggtgaaaattggaggaaccaacgcagaagtgtgc	689
Qy	683	accgcgcctgcgttatgctgggtcaagattacaggaacaaatgtgcaggatgcctg	742
Db	690	cccaagtggagttccaggtggaccgtgcgaaggattggatggggatcacctctg	749
Qy	743	cccaagtggaaattccaaataggacccctgtgaaggaaatccgcattggggatcatctctgg	802
Db	750	tagcacgttccatcccccacgggtgtgcgaagactttgggtcattgtgtccttcgatc	809
Qy	803	tggcccggttccatcttcgcattgtgaagactttgggtaatagcaaccccttgacc	862
Db	810	ccaaaccatccctggaaactggAACGGTGTGCACACCAACTCAGCACCAAGA	869
Qy	863	ccaaaccatccctggaaactggAACTGGTGCAGGCTGCCATACCAACTTAGCACCAAGG	922
Db	870	acatggggaaagatggggatcaagcacatcgaggaggccatcgagaagctgagcaagc	929
Qy	923	ccatgcggggaggaaatgggttgcaggacatcgaggaggccatcgagaaactaagcaagc	982
Db	930	gccaccaggtaaccacatccgtgcctacgaccccaaaggagggtggacaacgcggc	989
Qy	983	ggcacccgttaccacattcgagcctacgatcccaaggggggctggacaatgcggcgtgg	1042
Db	990	tgacgggcttccacggagacgtccacgcattccacagttctccggcggtggccaaacgg	1049
Qy	1043	tgactgggttccacgaaacgtccacatcaacgtttctgtgtgtcgccaaatcgca	1102
Db	1050	gcgcgcacatccgcatcccacgcaacgtggccatgagaagaaaggctacttcgaggacc	1109
Qy	1103	gtgcgcacatccgcattcccccggactgtcgccaggagaagaaaggtaactttaagacc	1162
Db	1110	gcgggccttcagccaaactgcgatccctacgcccgtgacggaggccctggtcgtacgt	1169
Qy	1163	gcgcgcgccttcgcattgtgaccccttgcagtgcacagaagccatgtccgcacatgcc	1222
Db	1170	tcctcaacgaaaccggggacggacccctttgagttacaagaactaagtggact	1220
Qy	1223	ttctcaatgagactggcgcacgagcccttccaatacaactaattagact	1273

Search completed: Fri Aug 8 16:45:36 1997  
 Job time : 2569 secs.

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MPsrch\_nn n.a. - n.a. database search, using Smith-Waterman algorithm  
Run on: Fri Aug 8 16:45:55 1997; MasPar time 133.41 Seconds  
984.006 Million cell updates/sec  
Tabular output not generated.  
  
Title: >N70819  
Description: (1-1419) from us08476567.seq  
Perfect Score: 1419  
N.A. Sequence: 1 ccgagccgagaatgggagta.....aatagaggagtcaagttctt 1419  
Comp: ggctcggtcttaccctcat.....ttatctcctcagttcaagaa  
  
Scoring table: TABLE default  
Gap 6  
  
Nmatch STD : Dbase 0; Query 0  
  
Searched: 121476 seqs, 46255616 bases x 2  
  
Post-processing: Minimum Match 0%  
Listing first 45 summaries .  
  
Database: n-geneseq26  
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7  
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13  
14:part14 15:part15 16:part16 17:part17 18:part18  
19:part19 20:part20 21:part21 22:part22 23:part23  
  
Statistics: Mean 9.364; Variance 4.957; scale 1.889

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query					Description	Pred.	No.	
	No.	Score	Match	Length	DB	ID			
c	1	1419	100.0	1419	2	N70819	Sequence encoding chi	0.00e+00	
	2	1187	83.7	13254	23	T40915	Nucleotide sequence o	0.00e+00	
	3	134	9.4	1429	1	N91849	Lettuce glutamine syn	2.62e-79	
	4	130	9.2	1255	1	Q05727	Gene encoding glutami	3.03e-76	
	5	131	9.2	1649	2	Q10333	Encodes Rice chloropl	5.20e-77	
	6	128	9.0	1200	1	Q05728	Gene encoding glutami	1.02e-74	
	7	127	8.9	1262	1	Q05729	Gene encoding glutami	5.95e-74	
	8	124	8.7	1338	2	N70758	Sequence encoding alf	1.16e-71	
	9	122	8.6	1068	2	N71176	Sequence encoding mut	3.86e-70	
	10	79	5.6	246	22	T26426	Human gene signature	5.44e-38	
	11	76	5.4	1047	2	Q10572	Human Natriuretic Pep	8.29e-36	
	12	77	5.4	1047	2	Q10572	Human Natriuretic Pep	1.56e-36	
	13	58	4.1	185	2	N70762	Partial sequence of t	5.56e-23	
	14	58	4.1	221	2	N70760	Partial sequence of t	5.56e-23	
	15	47	3.3	1200	1	N90907	Glutamine synthesis g	1.84e-15	
	16	45	3.2	91	9	Q51746	Oligonucleotide probe	3.93e-14	
	17	46	3.2	4464	2	N71244	Genomic sequence of a	8.53e-15	
	18	46	3.2	4465	5	Q28697	Glutamine synthetase.	8.53e-15	
	c	19	43	3.0	91	9	Q51746	Oligonucleotide probe	8.14e-13
	c	20	42	3.0	204	1	N81164	Base substituted E.co	3.66e-12
	21	43	3.0	312	2	N70764	Partial sequence of t	8.14e-13	
	22	41	2.9	204	1	N81164	Base substituted E.co	1.63e-11	
	23	37	2.6	348	6	Q39897	Expressed Sequence Ta	5.78e-09	
	24	37	2.6	348	8	Q59309	Human brain Expressed	5.78e-09	
	25	36	2.5	114	12	Q70467	Generic DNA sequence	2.44e-08	
	26	34	2.4	48	18	T13986	Glutamine synthetase	4.19e-07	

27	34	2.4	114	12	Q70468	Generic DNA sequence	4.19e-07	
28	34	2.4	114	12	Q70465	Generic DNA sequence	4.19e-07	
29	33	2.3	114	12	Q70470	Generic DNA sequence	1.70e-06	
30	32	2.3	114	12	Q70472	Generic DNA sequence	6.80e-06	
31	32	2.3	114	12	Q70469	Generic DNA sequence	6.80e-06	
c	32	2.3	114	12	Q70469	Generic DNA sequence	6.80e-06	
c	33	32	2.3	114	12	Q70468	Generic DNA sequence	6.80e-06
34	33	2.3	200	2	N70759	Partial sequence of t	1.70e-06	
35	31	2.2	114	12	Q70471	Generic DNA sequence	2.68e-05	
c	36	31	2.2	114	12	Q70467	Generic DNA sequence	2.68e-05
37	30	2.1	114	12	Q70466	Generic DNA sequence	1.04e-04	
c	38	30	2.1	114	12	Q70470	Generic DNA sequence	1.04e-04
c	39	30	2.1	114	12	Q70465	Generic DNA sequence	1.04e-04
c	40	30	2.1	501	3	N50023	Sequence encoding new	1.04e-04
41	29	2.0	114	12	Q70473	Generic DNA sequence	3.95e-04	
c	42	29	2.0	114	12	Q70466	Generic DNA sequence	3.95e-04
c	43	28	2.0	501	3	N50026	Sequence encoding new	1.48e-03
c	44	28	2.0	501	3	N50033	Sequence encoding new	1.48e-03
c	45	26	1.8	114	12	Q70471	Generic DNA sequence	1.94e-02

### ALIGNMENTS

RESULT 1  
ID N70819 standard; cDNA; 1419 BP.  
AC N70819;  
DT 13-MAY-1991 (first entry)  
DE Sequence encoding chinese hamster glutamine synthetase.  
KW DHFR/MTX; ss.  
OS Cricetus griseus.  
FH Key Location/Qualifiers  
FT stem\_loop 7..80  
FT /\*tag= a  
FT stem\_loop 81..130  
FT /\*tag= b  
FT CDS 145..1266  
FT /\*tag= c  
PN WO8704462-A.  
PD 30-JUL-1987.  
PF 23-JAN-1987; GO0039.  
PR 23-JAN-1986; GB-001597.  
PA (CELL-) CELLTECH LTD.  
PA (UNIU ) UNIV OF GLASGOW.  
PA (WILS/) WILSON RH.  
PI Wilson RH, Bebbington CR;  
DR WPI; 87-221263/31.  
DR P-PSDB; P70501.  
PT Recombinant DNA which encodes glutamine synthetase - used esp. in  
PT co-amplification of non-selected genes and in transforming host  
PT cell lines.  
PS Claim 6; Fig 2a-e; 54pp; English.  
CC Sequence may be used as a hybridisation probe in the isolation of the  
CC GS gene in other species, and as a diagnostic tool in the detection  
CC of diseases altering GS expression. A second use is as a selectable  
CC marker in recombinant DNA technology eg. co-amplification selection,  
CC or transformation to glutamine independence.  
SQ Sequence 1419 BP; 338 A; 391 C; 361 G; 329 T;

Query Match 100.0%; Score 1419; DB 2; Length 1419;  
Best Local Similarity 100.0%; Pred. No. 0.00e+00;  
Matches 1419; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1 ccgagccgagaatgggagtagagccactgcttgcattccacccaatctcctcgccgt 60  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 1 ccgagccgagaatgggagtagagccactgcttgcattccacccaatctcctcgccgt 60  
Db 61 ctcacttcgcctcggtctcggtggctcggtggccctgtccaccccggtcatcatcccgccgg 120  
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Qy 61 ctcacttcgcctcggtctcggtggctcggtggccctgtccaccccggtcatcatcccgccgg 120  
Db 121 ccaccgctcagagcacccatggccacctcagcaagtcccacttgaacaaaaac 180  
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Qy 121 ccaccgctcagagcacccatggccacctcagcaagtcccacttgaacaaaaac 180  
Db 181 atcaagcaaatgtacttgcctgccccagggtgagaaagtccaagccatgtatatctgg 240